

**Plot of lcl|31669 vs gi|42541062|gb|AAS19428.1|**

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

Descriptions

		Score	E
Sequences producing significant alignments:		(Bits)	Value
<a href="#">gb AAS19428.1 </a>	anti-SARS S protein immunoglobulin light chain...	144	4e-40

Alignments [Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) [NEW](#)

>[gb|AAS19428.1|](#) anti-SARS S protein immunoglobulin light chain variable region  
[Homo sapiens]  
Length=106

Score = 144 bits (362), Expect = 4e-40, Method: Compositional matrix adjust.  
Identities = 70/104 (67%), Positives = 85/104 (81%), Gaps = 0/104 (0%)

Query	4	MTQSPSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHAGVPSRFS	63
		MTQSPSSLSAS+GDRVTII+CRA+Q IS +LNWYQQ+ KLLIY S L +GVPSRFS	
Sbjct	3	MTQSPSSLSASVGDRTITCRATQSISTHLNWYQQRGGKAPKLLIYGASTLESGVPSRFS	62
Query	64	GS GSGTDYSLTISNLEQEDIATYFCQQGYTLPTYFGGGTKLEIK	107
		GS GSGT+++LTIS+L+ ED ATY+C Q + P+TFG GT +EIK	
Sbjct	63	GS GSGTEFTLTISLQPEDFATYYCLQHRYPWTFGQGGINVEIK	106

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